



KAROLINSKA INSTITUTET
- a medical university -

EXHIBIT 1

Department of: CLINICAL IMMUNOLOGY

Laboratory Journal No: .

Name: ~~XXXXXXXXXX~~
HANS GRENBLUND

Group:

Date: [REDACTED]
from to



cont. from page no:

Study

cont. on page no:

Project no.

Study no.

27

Assembly of a synthetic gene coding for
Tel d1 Chain 1 using Tag

PCR

Oligos 132, 133, 134, 135 10 μ M

1 μ l of each oligo 132-135

1 μ l dNTP 10 mM

0.5 μ l Tag

1 μ l 10x Tag-buffer

3.5 μ l H₂O

10 μ l

→ PCR Eppendorf program HAN51

94°C 1 min

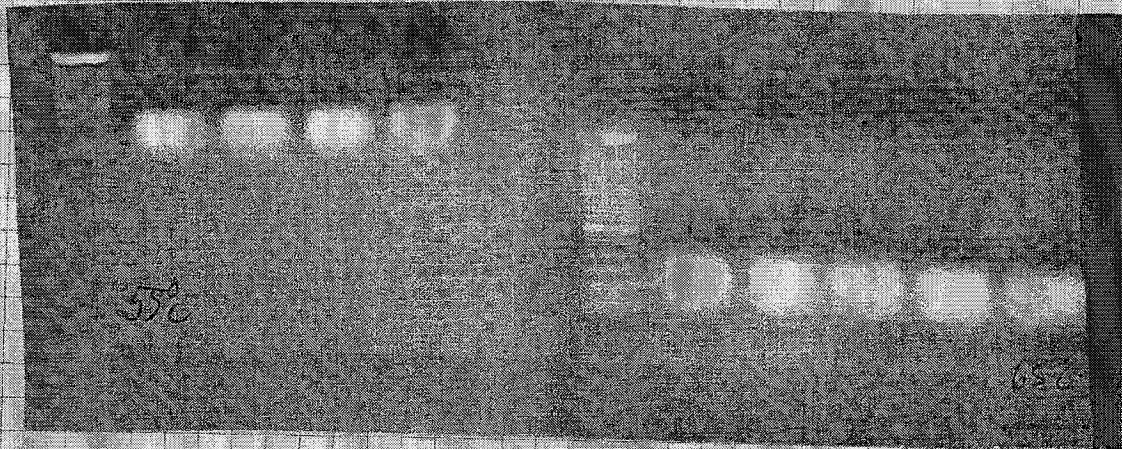
annealing 65-65°C 1.5 min (grad)

elongation 68°C 20 min

30 cycles ending 10 min elongation

+ 4°C

Result A strong band around 300 (exp. ~ 200)



Read and understood by

Signature

Date

Signature

Date



Laboratory Journal

248910

cont. from page no.

Study

Assembly of chain 2 Fel d1

cont. on page no.

Project no.

Study no.

primers 127-131 + 138

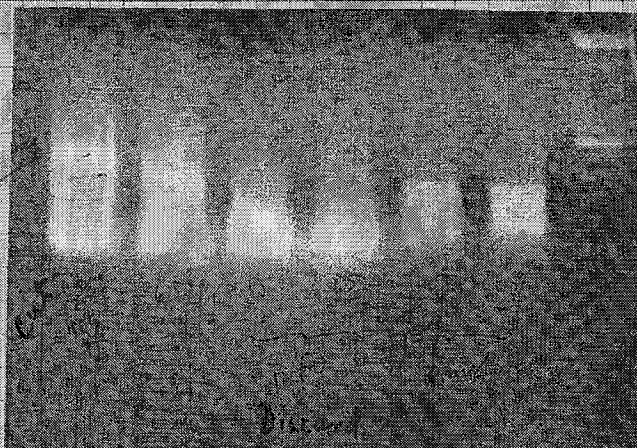
Using 3 different DNA polymerases

Method as: assembly chain 1"

Tag
pfu

Ampli Tag

expected band
at 294



to 248913
Lane 1

Read and understood by

Signature

Date

Signature

Date



cont. from page no:

Study

Expression and purification of
Feld1 chain 1 and chain 2.

cont. on page no:

Project no.

Study no.

Feld1 chain 1 (clone 42) and Feld1 chain 2 clone 29 was ligated into pET 20b and electroporated into BL-21 DE3 pLysS after having been cut from pT7-Blue containing the correct sequence. (see binder HG1, Feld1) Sequencing of pET 42/pET 29 was done according to standard protocol (ABI) and the results can be seen on the opposite side.

Both Feld1 chain 1 (Fd1:1) and Feld1 chain 2 (Fd1:2) was expressed according to standard protocol and purified on a HiTrap (chelex) column loaded with NiSO₄.

Chain 1 was soluble, after ultra sonication chain 1 was found in 20 mM Tris-HCl pH fraction, while chain 2 was found in the inclusion bodies after "washing" with 2M urea buffer + 20 mM Tris-HCl pH 8.0. The inclusion bodies were solubilized in 6M guanidine, transferred to 6M urea buffer (20 mM Tris-HCl pH 8.0 + 0.5M NaCl) via 6M Tris-HCl trap. Purification was done on FPLC

Read and understood by

Signature

Date

Signature

Date

test serie/analyse Blad 1 Allegat II

Personnummer	knr	g.1	et prick	
340217-3235	29	0.47		Amphiox
370413-3218	59	11.4	3	Amphiox
380620-1236	50	8.2	3	
419317-3210	95	1.24		
429508-3215	102	2.21		
471013-3254	110	0.43		
430308-3277	118	1.3		
441118-3272	135	1.03	2	
471031-3273	172	1.07		
480710-3218	193	0.82		
500228-3217	203		2	
500615-3233	234	0.73		
510414-3231	235		2	
511020-3212	250	0.84	3	
531018-3232	243	0.37		
531108-3235	245	0.85	2	
540209-3214	253		2	
540823-3232	251	87.7		
550521-3213	272	26.5	2	
560701-3218	283	0.65		Amphiox
570415-3211	285	0.65		
580611-3215	317	0.82	2	
600623-3215	341		2	
640316-3216	385	2.06		
621110-3255	378		2	
650127-3212	380		2	
630703-3230	388	1.56		
640724-3234	398	0.47		
660628-3210	403		2	
680828-3212	406	0.76		
680703-3241	416	3.06	2	
671004-3256	422	26.5	3	Amphiox
680220-3213	426		2	
680520-3210	428	0.50		
690108-3235	434	21.45	3	Amphiox
730812-3251	452	5.33		
740300-0044	454	8.33	2	Amphiox
740313-3213	455	0.36		
750108-3210	458	17.1	3	

Ex 31

C:\program\genesis\protocolab\307\NOV00V.004

LABSYSTEMS GENESIS 1.0.0.17
 Raw data filename: c:\program\genesis\protocolab\307\NOV00V.004
 Processed by Protocol: c:\program\genesis\protocolab\307\NOV00V.004
 Plotter layout file: c:\program\genesis\protocolab\307\NOV00V.004
 Reading type: Dual Wavelength
 Instrument version: Multiskan RC V.1.0
 Filter 1: 405nm
 Filter 2: 520nm
 Scan time: 00:00:10
 Interval between edge: 00:00:10
 Mix: YRS
 Mix RPM: High
 Mix ON period: 00:00:05
 Mix OFF period: 00:00:05
 Wavelengths:
 405 nm 520 nm

Raw data values (calculated):	1st	2nd	3rd	4th	5th	6th	7th	8th	9th	10th	11th	12th
A	0.049	0.057	0.143	0.142	1.355	0.637	0.937	0.253	0.197	0.088	0.178	0.040
B	0.046	0.053	0.115	0.095	1.463	0.689	0.643	0.145	0.105	0.083	0.144	0.117
C	0.050	0.051	0.178	0.156	1.137	0.449	0.304	0.988	0.114	0.020	0.158	0.103
D	0.054	0.055	0.182	0.105	1.182	0.776	0.757	0.118	0.175	0.085	0.145	0.102
E	0.054	0.113	0.064	0.059	0.851	0.411	2.404	1.092	0.114	0.028	0.148	0.094
F	0.054	0.042	0.056	0.234	0.837	0.532	0.477	1.118	0.111	0.043	0.179	0.084
G	0.063	0.050	0.240	0.106	1.435	0.823	0.607	0.258	0.182	0.080	0.182	0.120
H	0.053	0.119	0.183	0.250	1.140	1.354	1.510	0.046	0.107	0.048	0.292	0.087

23 33 273 423 453 24 454
 11.4 285 26.5 2145 8.3

Amphiox

Comments:

Plate 1: 45 min

Raw data values (calculated):	1st	2nd	3rd	4th	5th	6th	7th	8th	9th	10th	11th	12th
A	0.049	0.057	0.143	0.142	1.355	0.637	0.937	0.253	0.197	0.088	0.178	0.040
B	0.046	0.053	0.115	0.095	1.463	0.689	0.643	0.145	0.105	0.083	0.144	0.117
C	0.050	0.051	0.178	0.156	1.137	0.449	0.304	0.988	0.114	0.020	0.158	0.103
D	0.054	0.055	0.182	0.105	1.182	0.776	0.757	0.118	0.175	0.085	0.145	0.102
E	0.054	0.113	0.064	0.059	0.851	0.411	2.404	1.092	0.114	0.028	0.148	0.094
F	0.054	0.042	0.056	0.234	0.837	0.532	0.477	1.118	0.111	0.043	0.179	0.084
G	0.063	0.050	0.240	0.106	1.435	0.823	0.607	0.258	0.182	0.080	0.182	0.120
H	0.053	0.119	0.183	0.250	1.140	1.354	1.510	0.046	0.107	0.048	0.292	0.087

Coating: A: 10mg/ml
 B: 5mg/ml
 C: 2.5mg/ml
 D: 1mg/ml



cont. from page no:

cont. on page no:

Study

Project no.

Study no.

Test of Fd1 chain 1 clone 92 and
Fd1 chain 2, clone 29 with 6 cat sensitized
Allogenic from Allog study

6 farnes from the Allog study, no 29, 59, 277, 422,
434 and 454,
was diluted 3 times and 10 times resp. in
PBS pH 7.4. A μ -titer plate was coated with:

Plate 1

A 10 μ g/ml chain 1 \rightarrow (All horizontal wells)
B 5 μ g/ml "
C 2.5 μ g/ml "
D 1.25 μ g/ml "
E 10 μ g/ml chain 2 \rightarrow
F 5 "
G 2.5 "
H 1.25 "

Plate 2

A 5+5 μ g/ml chain 1+2 (a 1:1 mix of resp chain
B 2.5+2.5 "
C 1.25+1.25 " Chain 1+2 with 5 μ g/ml each)

On the vertical rows the patients were added

	1	2	3	4	5	6	7	8	9	10	11	12
	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓	↓
Patient	29		59		277		422		434		454	
	3x	10x	3x	1x								

Read and understood by

Date

Signature

Date



cont. from page no.

cont. on page no.

Study

Project no.

Study no.

(cont.)

ELISA conditions

Coating of Fd 1:1 and Fd 1:2 ^(100 µl/well) over the weekend in +4°C. Serum 4 times was with "Tris coating". Patients serum was added, 100 µl/well and incubated at +4°C o.n. Wash 4 times (Wallac ELISA-washer) with "Tris coating" and 100 µl Rabbit/human ~~anti~~ IgG del 1000 times in "Vär buffert". Incubation 2 hours in RT on shaker, Wash 4x "Tris coating" and add 100 µl/well of Goat anti-rabbit-ALP conjugated (DAKO) for 1h. Wash 4 times and add substrate 3 tablets/15ml of Vär buffert.

The result was read in ELISA reader after 45 min at 405 ~~nm~~ nm

Result: 2.5 µg/ml seems to be an adequate coating concentration for both chain 1 and chain 2. Mixing of the two chains can be done with coating concentrations 2.5 + 2.5 µg/ml

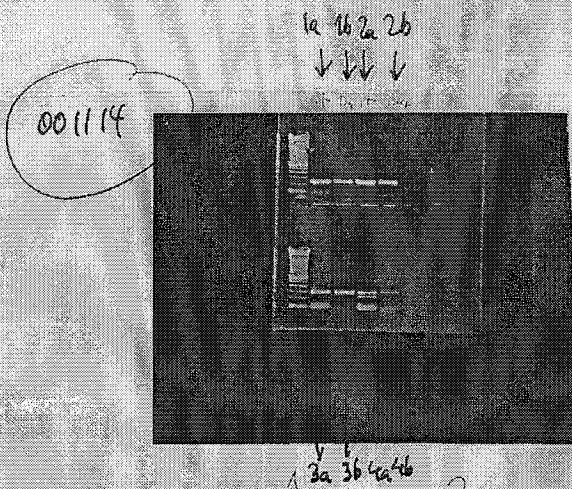
Read and understood by

Signature

Date

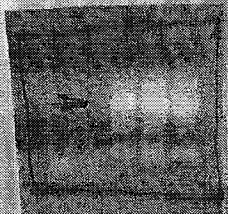
Signature

Date



Putting chain 1 and 2 (1+2)
together (001121)

template 1a 6µl
template clone 29 1µl
1:10, 1:100, 1:1000
0.5µl primer 176
2µl — — 183
2µl dNTP
3µl 10x buff.
1µl pfu
14.5µl H₂O
30µl



Result: One band
of ~500bp which
could be chain 1+2

↓
The bands are cut
out and purified
on Qiaquick

↓
ligated with "perfectly home
cloning kit". 10 colonies
are picked for miniprep
and possibly sequencing

1a 1µl template clone 11.42 (1:1000)
2µl primer 176
2µl — — 183
2µl 10x buff
1µl pfu
2µl dNTP (10mM)
10µl H₂O
20µl

1b Same as 1a, but
primer Tag polymerase

2a 1µl templ. (1:1000) clone 11.42
1µl templ. — — clone 29
2µl primers. 176, 183, 183
overnight same 1a

2b Same 2a with Tag

3a 1µl template clone 2 (1:1000)
2µl 183
2µl 175
overnight same 1a

3b Same 3a with Tag

4a 1µl templ. 1
1µl templ. 2
2µl primer 186
overnight same 3a

4b Same 4a with Tag

AmpliTaq Gold
250 Units, 5U/µl
Store at -20 °C

Lot No. 0000000000
A03912



cont. from page no:

cont. on page no:

Study

Linking of (chain 1 and chain 2 (seamless))
with PCR Fd1:1 and Fd1:2

Project no.

Study no.

Aim. The aim of this experiment is to join the two chains of Fd1 into one construct by PCR

Study outline The two sequenced chains of the major chains of cat Fd1 (chain 1, clone 42) and chain 2, clone 29) is joined with PCR in two steps as outlined below. In



Result (see opposite side)

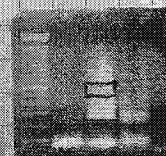
Good bands of expected size was seen for both chain 1 and chain 2. But (2a) and (2b) as well as (4a) and (4b) did not work. I will continue by adding (1a) to ~~template~~ 29 and to PCR. (chain 1+2)



PCR: 5' (1+2)
1st templ. ch2 (1:1000)
2nd 186
3rd 184
→ did not work

PCR primers 180, 181

PCR: 5' (2+1)
1st templ. chain 1 (1:1000)
Chain 2 (1:1000)
1st 181
2nd 181
3rd 180
4th pfu
5th 10x buff
6th 180
→ 5.30µl



cut band

Read and understood by

Signature

Date

Signature

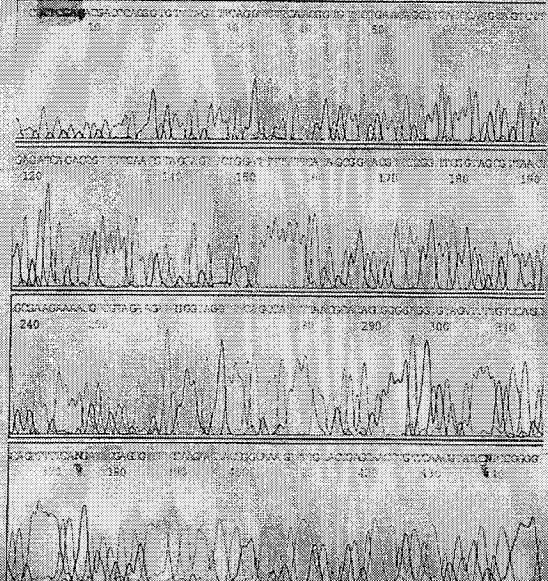
Date

PRISM

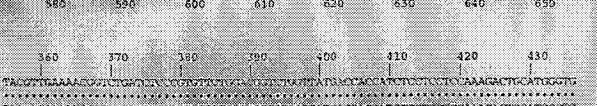
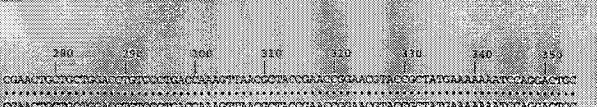
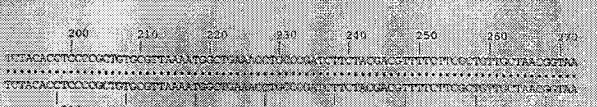
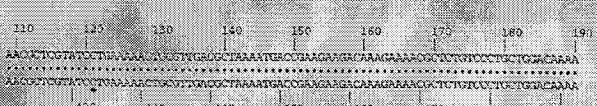
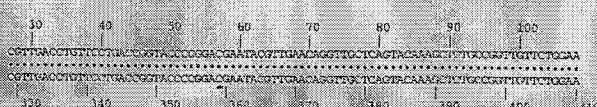
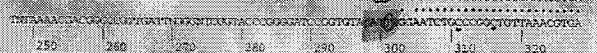
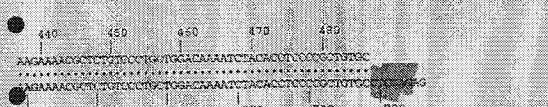
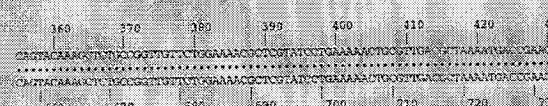
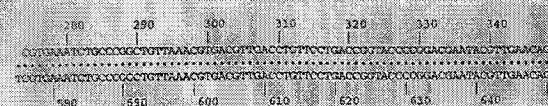
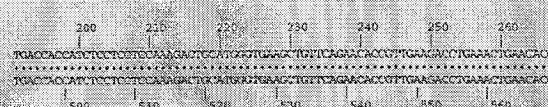
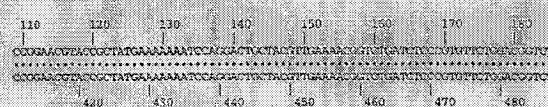
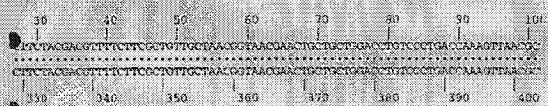
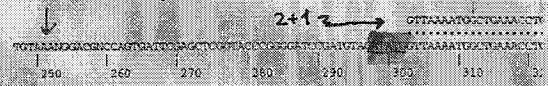
ABI106
Version 3.2

File 20
Lane 22

Seq 000
Points 19



Ed1 (2+1) PT7 d1R 001205 (t+term.)



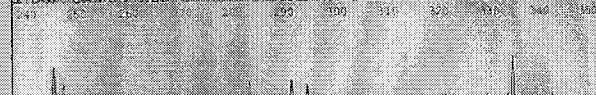
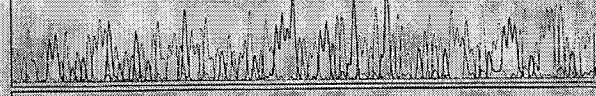
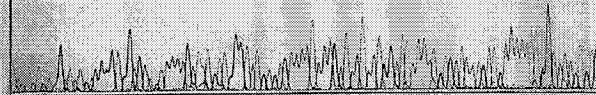
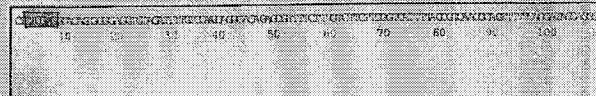
ABI
PRISM

Model 377
Version 3.4
ABI106
Version 3.2

File 20
Lane 22

Signal G112 A183 C111 T126
DT (dB) Set Any Primer
Seq diff 0.18 extra
Points 1335 to 8260 Pk 11 loc 1335

man 4 dec 8
man 4 dec 2
Spacing





cont. from page no.

cont. on page no.

Study

Project no.

Study no.

Sequencing of 4 clones of each 1+2 and 2+1.

1+2	clone no	seq no
	↓	↓
Clone 1	= ①	
2	= ②	
5	= ③	OK seq
9	= ④	

2+1

Clone	1	5
6	⑤	OK seq red - prom
7	⑥	OK seq black - term.
9	⑦	OK seq (prom. seq)
	⑧	

4.8 µl vector
1.2 µl primers
4 µl mix BD after dehydroamino
10 µl

+ 50 µl oil and

PCR p₀ Perkin Elmer

98°C	30"
50°C	15"
60°C	4'

 } 25 cycles

Unfortunately there was a scheduled power failure and the PCR-run was interrupted. Assume 7 more cycles which is done....

Samples are loaded on lanes 20 - 33 on ABI seq and named

Fd 1	1+2	pT7	clone	4F
-	"	-	-	4R
-	"	-	-	5F
-	"	-	-	5R
				etc.

Cloning of clone 5 (1+2) and clone 1 (2+1) with NotI and XhoI for ligation into pET 20b

20 µl plasmid miniprep (pT7 Blue)

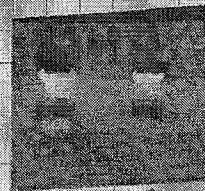
2.4 µl 10x buff

0.3 µl BSA

0.7 µl NotI

0.7 µl XhoI

Incubate 37°C shake for 2h.



Diagonal point.

↑	↑
clone	clone
1(2+1)	5(1+2)

Read and understood by

Signature

Date

Signature

Date



cont. from page no.

cont. on page no.

Study

Ligation of Fd 1, clone 1 (2+1) and clone 5 (1+2)
into pET 20b+ and electroporation into BL21 plys

Project no.

Study no.

The fragments from Fd 1 (2+1) clone 1 and clone 5 (1+2)
were Qigen purified from 1% agarose gel (248931)
A cleaned (Nde/Xho) pET 20b+ vector was used
to ligate the fragments

Conclusions

12 μ l ~~vector~~ fragments
10 μ l vector
1.5 μ l 10 mM ATP
1.8 μ l 10x ligase buffer
1.7 μ l T4 ligase
18 μ l

Ligate +16°C o.n.

The ligate mix was electroporated into 50 μ l BL21-
-plys electrocompetent cells. 1 μ l ligate mix
was added to thawed cells (on ice). Electroporation
according to standard protocol. Growth on SOC
medium for 60' 37°C shaker (300 rpm) and
plated on Amp/CAN plates. One colony ~~from~~
each plate was picked and grown on LB Amp
CAN medium, mini prepped (Qigen)
and 25 μ l of the (50 μ l) prep was
cut with Nde and Xho. Result ~ 800bp
Both clones contain the insert!!



Read and understood by

Signature

Date

Signature

Date



cont. on page no:

Project no:

Study no:

Purification of Fd1 (1+2) clone 5 and
Fd1 (2+1) clone 1 over Ni^{2+} chelate thi-Trap

1 liter of Fd1 (1+2) and (2+1) ^{in PET 206 in BL-2 (Phys)} resp. LB-medium (CAM, Amp)
was grown to OD 0.6 (600nm) and induced with
0.4 mM IPTG. (see 248932)

Purification according to protocol. Both proteins
were expressed as inclusion bodies and
purified accordingly ~~and~~ Purification on FPLC
as follows. After adsorption onto thi-column in
6M Urea and wash also with 6M Urea the
column is stuck to FPLC

Program:

0 conc % B 0

0 ml/min 5.0 ml/min

0 0.25 ml/min

0 port set 6.1

20 conc % B 0

80 conc % B 100

100 conc % B 100

125 conc % B 0

125 port set 6.0

A = 6 M Urea

B = 20 mM Imidazole

C = 500 mM Imidazole



Read and understood by

Signature

Date

Signature

Date